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Title: US-08-569-749-5
 Run on: January 7, 2002, 16:03:52 ; Search time 180.87 seconds
 Perfect score: 307 (without alignments)
 Sequence: CELYRNMSTVSTPFAGVPVSE.....KVKCFCGILMDNWKLGDSP 55
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
 Minimum DB seq length: 0 (without alignments)
 Maximum DB seq length: 200000000
 Total number of hits satisfying chosen parameters: 473505

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPREMBL_17: *
 1: sp_archea: *
 2: sp_bacteria: *
 3: sp_fungi: *
 4: sp_human: *
 5: sp_invertebrate: *
 6: sp_mammal: *
 7: sp_mmc: *
 8: sp_organelle: *
 9: sp_phage: *
 10: sp_plant: *
 11: sp_rhodent: *
 12: sp_virus: *
 13: sp_vertebrate: *
 14: sp_unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|--------|-------------|
| 1 | 301 | 98.0 | 1140 4 | Q03UH1 |
| 2 | 298 | 97.1 | 602 11 | Q9ES99 |
| 3 | 291 | 94.8 | 589 11 | Q9ZC66 |
| 4 | 291 | 94.8 | 589 11 | Q9ES88 |
| 5 | 247 | 80.5 | 324 13 | Q9DD00 |
| 6 | 247 | 80.5 | 610 13 | Q57319 |
| 7 | 152 | 49.5 | 496 11 | Q9ES97 |
| 8 | 152 | 49.5 | 501 11 | Q9EB05 |
| 9 | 152 | 49.5 | 501 11 | Q9ED04 |
| 10 | 155 | 47.2 | 264 12 | Q9ENZ7 |
| 11 | 143 | 46.6 | 195 13 | Q9IA10 |
| 12 | 143 | 46.6 | 197 13 | Q9IA09 |
| 13 | 140 | 45.6 | 281 12 | Q9YN18 |
| 14 | 134 | 597 | 111 | Q9R015 |
| 15 | 131 | 42.7 | 224 11 | Q986542 |
| 16 | 127 | 41.4 | 438 12 | Q9A505 |
| 17 | 119 | 36.8 | 208 12 | Q55770 |
| 18 | 117 | 38.1 | 280 12 | Q9RAF7 |
| 19 | 117 | 38.1 | 298 4 | Q9R2A8 |

Pred. No. is the number or results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | | |
|---------------------------------|---|---------------------------------------|--|-------------------------|---|
| SO | SEQUENCE | 1140 AA: | 128738 MW: | 0C18D890287C723E CRC64: | |
| Query Match | 98.0% | Score 301; | DB 4; | Length 1140; | RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."; |
| Best Local Similarity | 98.2% | Pred. No. | 5 | Indels 0; | RL Submitted (SPR-1999) to the EMBL/GenBank/DDBJ databases. |
| Matches | 54; | Mismatches | 1; | Gaps 0; | CC -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. |
| Qy | 1 CELYRMSTYSPAGVPSERSLARAGFYVTGNDVKFCFCGLMLDNWKLGDSP 55 | EMBL; AF190020; AK025851; -; | DR HSSP; Q11490; 1QBH; | | |
| Db | 28 CELYRMSTYSPAGVPSERSLARAGFYVTGNDVKFCFCGLMLDNWKLGDSP 82 | DR InterPro; IPR001370; BTR; | DR InterPro; IPR001315; Znf_ring. | | |
| RESULT | 2 | DR pfam; PF00655; BIR; 3; | DR pfam; PF00619; CARD; 1; | | |
| ID | Q9SE99 | DR Pfam; PF00097; zf-C3HC4; 1. | DR InterPro; IPR001841; Znf_ring. | | |
| AC | Q9SE99 | DR SMART; SM00238; BIR; 3; | DR PROSITE; PS01282; BIR_REPEAT_1; 3. | | |
| DT | 01-MAR-2001 (TREMBL); 16, Last sequence update) | DR SMART; SM00114; CARD; 1. | DR PROSITE; PS01283; BIR_REPEAT_2; 3. | | |
| DT | 01-JUN-2001 (TREMBL); 17, Last annotation update) | DR SMART; SM00184; RING; 1. | DR PROSITE; PS01209; CARD; 1. | | |
| DE | INHIBITOR OF APOPTOSIS PROTEIN 1. | DR Zinc-fingerer. | KW SEQUENCE: 589 AA; 66777 MW; E6812FFB3EA34142 CRC64; | | |
| OS | Rattus norvegicus (Rat); | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | | |
| OX | NCBI_TaxId=1016; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Holick M., Lefebvre C.A., Hicks K., Korneluk R.G.; | | | | |
| RT | Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.", | | | | |
| RT | Submitted (SPR-1999) to the EMBL/GenBank/DDBJ databases. | | | | |
| RL | | | | | |
| CC | -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. | | | | |
| EMBL; AF183430; AK022970; 1; -; | | | | | |
| DR | InterPro; IPR001370; BIR. | | | | |
| DR | InterPro; IPR001315; CARD. | | | | |
| DR | Znf_ring. | | | | |
| DR | PRO0055; BIR; 3; | | | | |
| DR | PFAM; PF00115; CARD; 1; | | | | |
| DR | PFAM; PF00097; zf-C3HC4; 1. | | | | |
| DR | SMART; SM00238; BIR; 3; | | | | |
| DR | SMART; SM00114; CARD; 1. | | | | |
| DR | SMART; SM00184; RING; 1. | | | | |
| DR | PROSITE; PS01282; BIR_REPEAT_1; 1. | | | | |
| DR | PROSITE; PS00504; BIR_REPEAT_2; 3. | | | | |
| DR | PROSITE; PS01209; CARD; 1. | | | | |
| DR | Zinc-fingerer. | | | | |
| RW | ZINC_FINGER. | | | | |
| SEQUENCE | 602 AA; 67326 MW; CC913B5EEA62DDE5A CRC64; | | | | |
| Query Match | 97.1% | Score 298; | DB 11; | Length 589; | RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."; |
| Best Local Similarity | 96.4% | Pred. No. 6 | 9e-30 | Indels 0; | RL Submitted (SPR-1999) to the EMBL/GenBank/DDBJ databases. |
| Matches | 53; | Mismatches | 1; | Gaps 0; | CC -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. |
| Qy | 1 CELYRMSTYSPAGVPSERSLARAGFYVTGNDVKFCFCGLMLDNWKLGDSP 55 | DR HSSP; Q11490; 1QBH; | DR InterPro; IPR001370; BTR; | | |
| Db | 28 CELYRMSTYSPAGVPSERSLARAGFYVTGNDVKFCFCGLMLDNWKLGDSP 82 | DR InterPro; IPR001315; Znf_ring. | DR InterPro; IPR001841; Znf_ring. | | |
| RESULT | 3 | DR pfam; PF00655; BIR; 3; | DR pfam; PF00619; CARD; 1; | | |
| ID | Q9QC66 | DR SMART; SM00114; CARD; 1. | DR SMART; SM00184; RING; 1. | | |
| AC | Q9QC66; | DR PROSITE; PS01282; BIR_REPEAT_1; 1. | DR PROSITE; PS01209; CARD; 1. | | |
| DT | 01-MAY-2000 (TREMBL); 13, Last sequence update) | DR Zinc-fingerer. | KW SEQUENCE: 589 AA; 66750 MW; B4F7089BD7CD285B CRC64; | | |
| DT | 01-MAY-2000 (TREMBL); 13, Last sequence update) | | | | |
| DT | 01-JUN-2001 (TREMBL); 17, Last annotation update) | | | | |
| DE | INHIBITOR OF APOPTOSIS PROTEIN 2. | | | | |
| OS | Rattus norvegicus (Rat); | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | | | |
| OX | NCBI_TaxId=1016; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Holick M., Lefebvre C.A., Hicks K., Korneluk R.G.; | | | | |
| RT | Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.", | | | | |
| RT | Submitted (SPR-1999) to the EMBL/GenBank/DDBJ databases. | | | | |
| RL | | | | | |
| CC | -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. | | | | |
| DR | EMBL; AF183431; AK022971; 1; -; | | | | |
| DR | SEQUENCE FROM N.A. | | | | |
| RA | Holick M., Lefebvre C.A., Hicks K., Korneluk R.G.; | | | | |
| RT | Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.", | | | | |
| RT | Submitted (SPR-1999) to the EMBL/GenBank/DDBJ databases. | | | | |
| RL | | | | | |
| CC | -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. | | | | |
| DR | EMBL; AF183431; AK022971; 1; -; | | | | |
| DR | InterPro; IPR001315; CARD. | | | | |
| DR | InterPro; IPR001370; BTR. | | | | |
| DR | Znf_ring. | | | | |
| DR | PRO0053; BIR; 3; | | | | |
| DR | PFAM; PF00619; CARD; 1. | | | | |
| DR | PFAM; PF00097; zf-C3HC4; 1. | | | | |
| DR | Zinc-fingerer. | | | | |
| RW | ZINC_FINGER. | | | | |
| SEQUENCE | 589 AA; 66750 MW; B4F7089BD7CD285B CRC64; | | | | |
| Query Match | 94.8% | Score 291; | DB 11; | Length 589; | RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."; |
| Best Local Similarity | 94.5% | Pred. No. 5 | 3e-29 | Indels 0; | RL Submitted (SPR-1999) to the EMBL/GenBank/DDBJ databases. |
| Matches | 52; | Mismatches | 3; | Gaps 0; | CC -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. |
| Qy | 1 CELYRMSTYSPAGVPSERSLARAGFYVTGNDVKFCFCGLMLDNWKLGDSP 55 | DR HSSP; Q11490; 1QBH; | DR InterPro; IPK001370; BTR; | | |
| Db | 24 CELYRMSTYSPAGVPSERSLARAGFYVTGNDVKFCFCGLMLDNWKLGDSP 78 | DR InterPro; IPK001315; Znf_ring. | DR InterPro; IPK001841; Znf_ring. | | |

| | | | |
|-----------------------|---|---|--------------|
| Db | 26 | EFNRUKTFANFPSSPPVSASTLARAGLYTGEDDVOGFSCHAAVDRWQYQDS | 78 |
| RESULT | 8 | | |
| ID | OQE005 | PRELIMINARY; | PRT; 501 AA. |
| AC | OQE005 | | |
| DT | 01-MAR-2001 | (TREMBLRL_16, Created) | |
| DT | 01-JUN-2001 | (TREMBLRL_17, Last sequence update) | |
| DE | | INHIBITOR OF APOPTOSIS PROTEIN 3, | |
| OS | | Rattus norvegicus (Rat). | |
| OC | | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OX | | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus. | |
| RN | [1] | NBII-TaxID:10116; | |
| RP | | SEQUENCE FROM N.A. | |
| RC | | SISTRANEWSTAR; TISSUE=OVARY; | |
| RA | Lareu R.R., Bradley C.K., Lacher M., Fritis R.R., Dharmarajan A.M.; | | |
| RT | "Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum"; | | |
| RU | Submitted (SEP 2000) to the EMBL/GenBank/DBJ databases. | | |
| CC | -1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. | | |
| EMBL: | AFO433; AUG41192; 1; -. | | |
| DR | InterPro: IPR001370; VIR_1; | | |
| DR | InterPro: IPR001841; Znf_fing. | | |
| DR | Pfam: PF00533; BIR_3; | | |
| DR | Pfam: PF00097; zf-C3HC4_1; | | |
| DR | SMART: SM00238; BIR_3; | | |
| DR | SMART: SM00184; RING_1; | | |
| DR | PROSITE: PS0143; BIR_REPEAT_1; 3; | | |
| KW | Zinc-finger; 501 AA; 56548 MW; 0973PBF20E81C5A0 CRC64; | | |
| SO | SEQUENCE | | |
| Query Match | 49.5% | Score 152; DB 11; Length 501; | |
| Best Local Similarity | 50.9% | Pred. No. 2.8e-11; | |
| Matches | 27; | Mismatches 18; Indels 0; | |
| PR | PRELIMINARY; | PRT; 501 AA. | |
| AC | OQE004 | | |
| DT | 01-MAR-2001 | (TREMBLRL_16, Created) | |
| DT | 01-MAR-2001 | (TREMBLRL_17, Last sequence update) | |
| DE | | INHIBITOR OF APOPTOSIS PROTEIN 3. | |
| OS | | Rattus norvegicus (Rat). | |
| OC | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC | | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus. | |
| OX | | NBII-TaxID:10116; | |
| RN | [1] | SEQUENCE FROM N.A. | |
| RP | | SEQUENCE FROM N.A. | |
| RC | | SISTRANEWSTAR; TISSUE=OVARY; | |
| RA | Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W., | | |
| RT | Moyer R.W.; | | |
| RU | Submitted (MAR 2000) to the EMBL/GenBank/DBJ databases. | | |
| CC | | | |
| EMBL: | AJ250284; AUG0727; 1; -. | | |
| DR | InterPro: IPR001370; VIR_1; | | |
| DR | InterPro: IPR001841; Znf_fing. | | |
| DR | Pfam: PF00533; BIR_2; | | |
| DR | SMART: SM00238; BIR_2; | | |
| DR | SMART: SM00184; RING_1; | | |
| DR | PROSITE: PS0143; BIR_REPEAT_2; 2; | | |
| SO | SEQUENCE | | |
| Query Match | 49.2% | Score 145; DB 12; Length 264; | |
| Best Local Similarity | 49.0% | Pred. No. 1.e-10; | |
| Matches | 25; | Mismatches 18; Indels 0; | |
| PR | PRELIMINARY; | PRT; 195 AA. | |
| AC | OQE010 | | |
| DT | 01-OCT-2000 | (TREMBLRL_15, Created) | |
| DT | 01-OCT-2000 | (TREMBLRL_17, Last sequence update) | |
| DE | | INHIBITOR OF APOPTOSIS 1 (FRAGMEN). | |
| OS | | Gallus gallus (Chicken). | |
| OC | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC | | Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; | |
| OX | | Gallus. | |
| RN | [1] | NBII-TaxID:9031; | |

| | | | |
|---|--|--|--|
| RP | SEQUENCE FROM N.A. | DE | IAP PROTEIN. |
| RC | STRAIN-BREED LEGION; TISSUE-SPLEEN; | GN | TAP. |
| RA | Zhou H., Lamont S.J.. | OS | Choristoneura fumiferana nuclear polyhedrosis virus (ChMNPV). |
| RT | "Genetic variation among chicken lines and mammalian species in specific genes." | OC | Viruses; dsDNA viruses, no RNA stage; Baculoviridae; |
| RT | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases. | OC | Nucleopolyhedrovirus. |
| DR | EMBL: AF221082; AAC55319.1; -. | NCBI_TAXID:10448; | [1] |
| DR | InterPro: IPR001370; BIR. | RP | SEQUENCE FROM N.A. |
| DR | Pram: PF0053; BIR; 2. | RC | STRAIN=IRELAND; |
| DR | SMART: SM0023; BIR; REPEAT_1; 2. | RA | Lauzon H., Arif B.M., Laad T., Balli R.; |
| DR | PROSITE: PSS0143; BIR_REPEAT_2; 2. | RT | "CIMMV IAP gene." |
| FT | NON_TER 1 | RL | Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases. |
| FT | SEQUENCE 195 AA: | CC | -; SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. |
| SQ | 195 AA: 22347 MW: 9C39BFA755E24E48 CRC64; | DR | EMBL: U82510; AAC00537.1; -. |
| Db | 119 RVKTFINPWRIPVQPEQPLQDAGFYYVGVGRNDVKCFCCDGGLRCWESGDDP 169 | DR | HSSP: Q1490; IQBR; |
| RESULT 12 | | DR | InterPro: IPR001370; BIR. |
| Q9IA69 | PRELIMINARY; PRT: 197 AA. | DR | PRAM: PR00653; BIR; 2. |
| ID Q9IA69 | DT 01-OCT-2000 (TREMBL); 15 (Created) | DR | PFAM: PR00097; zf-C3H4; 1. |
| AC Q9IA69; | DT 01-JUN-2001 (TREMBL); 17 (Last annotation update) | DR | SMART: SM0023; BIR; 2. |
| DE INHIBITOR OF APP/PROS1 (FRAGMENT). | DR | PROSITE: PS0128; BIR; REPEAT_1; UNKNOWN_1. | |
| OS Gallus gallus (Chicken). | DR | PROSITE: PS0143; BIR; REPEAT_2; 2. | |
| OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Gallus. | DR | ZINC-FINGER. | |
| OC NCBI_TaxID:9031; | DR | SEQUENCE 281 AA; 32090 MW; B2D9BEBR359F105E CRC64; | |
| RN [1] | | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| RP | SEQUENCE FROM N.A. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; |
| RC STRAIN-BREED FAYOMI; TISSUE-SPLEEN; | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| RA Zhou H., Lamont S.J.. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| RT "Genetic variation among chicken lines and mammalian species in specific genes." Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| DR EMBL: AF221082; AAC55320.1; -. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| DR InterPro: IPR001370; BIR. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| DR Pram: PF0053; BIR; 2. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| DR SMART: SM0023; BIR; 2. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| DR PROSITE: PS0128; BIR; REPEAT_1; 2. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| DR PROSITE: PS0143; BIR; REPEAT_2; 2. | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| FT NON_TER 1 | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| FT SEQUENCE 197 AA; 22602 MW; D79223ABC623E1A CRC64; | DR | Query Match Similarity 45.6%; Score 140; DB 12; Length 281; Best Local Similarity 48.1%; Pred No. 5; Jee-10; Matches 20; Indels 0; Gaps 0; | |
| RESULT 13 | | Query Match Similarity 45.6%; Score 143; DB 13; Length 197; Best Local Similarity 51.0%; Pred No. 1; Jee-10; Matches 20; Mismatches 5; Indels 0; Gaps 0; | |
| Q9NL8 PRELIMINARY; PRT: 281 AA. | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; | |
| ID Q9NL8 | AC Q9NL8; | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; |
| AC Q9NL8; | DT 01-MAY-1999 (TREMBL); 10 (Created) | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; |
| DT 01-MAY-1999 (TREMBL); 10 (Last sequence update) | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; | |
| Db 120 RVKTFINPWRIPVQPEQPLQDAGFYYVGVGRNDVKCFCCDGGLRCWESGDDP 170 | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; | |
| RESULT 13 | | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; | |
| Q9NL8 PRELIMINARY; PRT: 281 AA. | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; | |
| ID Q9NL8 | AC Q9NL8; | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; |
| AC Q9NL8; | DT 01-JUN-2001 (TREMBL); 17 (Last annotation update) | DR | Query Match Similarity 43.6%; Score 134; DB 11; Length 597; Best Local Similarity 46.3%; Pred No. 6; Jee-09; Matches 25; Conservatve 6; Mismatches 23; Indels 0; Gaps 0; |

Db 232 EELRMDMFKDMPOESPVGVEALVRAFFYTGKKDIVRCFSGGCLEKWAEGDDP 285

RESULT 15
 088642 PRELIMINARY; PRT: 224 AA.
 ID 088642;
 AC 088642;
 DT 01-NOV-1998 (TREMBLel 08, Last sequence update)
 DT 01-JUN-2001 (TREBLel 17, Last annotation update)
 DE INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
 GN RIPL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Rattus.
 OX NCBI_TaxId-10116;
 RN 11;
 RP SEQUENCE FROM N.A.

RC STRAIN=WT2R; TISSUE=Ovary; CORPUS LUTEUM;
 RA Lareu R.R.; Dharmarajan A.M.;
 RT "Cloning and characterisation of an inhibitor of apoptosis protein
 (IAP) in the rat corpus luteum.", submitted (ANG-998) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF001503; AAC:2497..1; -.
 DR HSSP; Q13490; 1QBH.
 DR InterPro; IPR001370; BXR.
 DR Pfam; PF00653; BIR; 2.
 DR SMART; SM00228; BIR; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 FT NON_TER 1
 FT NON_TER 224 1
 FT SEQUENCE 224 AA; 224 MW; 213A52534D5BB56A CRC64;

Query Match 42.7%; Score 131; DB 11; Length 224;
 Best Local Similarity 55.0%; Pred. No. 5.9e-09;
 Matches 26; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
 Ov 5 RMSTVSTFPAGVPSERSLARAGVYTGKVNDVKCFCGGLMIDNNWKLGDSP 55
 Db 173 RMTRFLWPPSSVLUQPEDLASAGFVYVHDNDVKCFCGCGLRWEPGDP 223

Search completed: January 7, 2002, 16:03:53
 Job time: 1412 sec